L Number	Hits	Search Text	DB	Time stamp
-	1	6163782.pn.	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:36
-	5	(("6035294") or ("6243699") or ("5930474") or ("5826261") or ("5692176")).PN.	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:37
-	1	bioinformatics adj data adj collection	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:39
-	1621	bioinformatics	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:41
-	1484	bioinformatics and (database or (data adj base))	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:40
-	53	bioinformatics adj database	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:50
-	103	(data adj collection) and taxonomy and category	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 10:52
-	23	((data adj collection) and taxonomy and category) and @rlad<=20000330	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 12:12
-	9	organism and (biological adj process) and (molecular adj function) and species and (cellular adj component)	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:27
-	149	(search adj engine) and taxonomy and category	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 12:22
-	40	((search adj engine) and taxonomy and category) and biolog$5	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 12:22
-	7	(((search adj engine) and taxonomy and category) and biolog$5) and @rlad<=20000330	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 12:22
-	0	707/3.ccls	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:28
-	2756	707/3.ccls.	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:28
-	69	707/3.ccls. and taxonomy	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:28
-	43	(707/3.ccls. and taxonomy) and category	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:28
-	0	((707/3.ccls. and taxonomy) and category) and @rlad<-20000330	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:28
-	69	707/3.ccls. and taxonomies	USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:29

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-	8	((707/3.ccls. and taxonomy) and category) and @rlad<=20000330		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:44
-	0	2001/0047353		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:44
-	1	"20010047353"		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:54
-	0	categorize adj search adj resutl		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:55
-	3	categorize adj search adj result		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/21 13:55
-	1			USPAT; US-PGPUB	2003/05/21 13:57
-	1			USPAT; US-PGPUB	2003/05/21 13:57
-	1			USPAT; US-PGPUB	2003/05/21 13:59
-	1			USPAT; US-PGPUB	2003/05/21 13:59
-	1			USPAT; US-PGPUB	2003/05/21 14:00
-	6	"6189013"		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/22 09:55
-	23	"6023659"		USPAT; US-PGPUB; EPO; JPO; IBM_TDB	2003/05/22 09:55

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1 Sequence similarity search and access methods: On the efficient   96%
evaluation of relaxed queries in biological databases
Yangjun Chen , Duren Che , Karl Aberer
**Proceedings of the eleventh international conference on Information and
knowledge management** November 2002
> In this paper, a new technique is developed to support the query relaxation in
> biological databases. Query relaxation is required due to the fact that queries tend not
> to be expressed exactly by the users, especially in scientific databases such as
> biological databases, in which complex domain knowledge is heavily involved. To treat
> this problem, we propose the concept of the so-called fuzzy equivalence classes to
> capture important kinds of domain knowledge that is used to relax queries. This co ...

2 Reports from KDD-2001: KDD Cup 2001 report   87%
Jie Cheng , Christos Hatzis , Hisashi Hayashi , Mark-A. Krogel , Shinichi Morishita , David
Page , Jun Sese
ACM SIGKDD Explorations Newsletter January 2002
Volume 3 Issue 2
> This paper presents results and lessons from KDD Cup 2001. KDD Cup 2001 focused
> on mining biological databases. It involved three cutting-edge tasks related to drug
> design and genomics.

3 Bioinformatics: BIOMIND-protein property prediction by property   85%
proximity profiles
Deendayal Dinakarpandian , Vijay Kumar
Proceedings f the 2002 ACM symp sium n Applied c mputing March 2002
> We present the infrastructure of a bioinformation system called BIOMIND, which
> exploits the close relationship between the *structural* and *functional* properties of

proteins. The scheme presented here views proteins as composite entities with structural and functional properties, and searches are based on distances along each property axis. Explicitly, this allows one to frame complex queries using quantitative criteria that confer more discerning power than systems based on a text-m ...

4 Poster session: A system for knowledge management in bioinformatics   84%
Sudeshna Adak , Vishal S. Batra , Deo N. Bhardwaj , P. V. Kamesam , Pankaj Kankar , Manish P. Kurhekar , Biplav Srivastava
Proceedings of the eleventh international conference on Information and knowledge management November 2002
> The emerging biochip technology has made it possible to simultaneously study expression (activity level) of thousands of genes or proteins in a single experiment in the laboratory. However, in order to extract relevant biological knowledge from the biochip experimental data, it is critical not only to analyze the experimental data, but also to cross-reference and correlate these large volumes of data with information available in external biological databases accessible online. We address this p ...

5 Background and overview for KDD Cup 2002 task 1: information   82%
extraction from biomedical articles
Alexander Yeh , Lynette Hirschman , Alexander Morgan
ACM SIGKDD Explorations Newsletter December 2002
Volume 4 Issue 2
> This paper presents a background and overview for task 1 (of 2 tasks) of the KDD Challenge Cup 2002, a competition held in conjunction with the ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD), July 23--26, 2002. Task 1 dealt with detecting which papers, in a set of fruitfly genetics papers (texts), contained experimental results about gene products (transcripts and proteins), and also within each paper, which genes had experimental results about their products me ...

6 Facilitating transformations in a human genome project database   82%
S. B. Davidson , A. S. Kosky , B. Eckman
Proceedings of the third international conference on Information and knowledge management November 1994
> Human Genome Project databases present a confluence of interesting database challenges: rapid schema and data evolution, complex data entry and constraint management, and the need to integrate multiple data sources and software systems which range over a wide variety of models and formats. While these challenges are not necessarily unique to biological databases, their combination, intensity and complexity are unusual and make automated solutions imperative. We illustrate these problems in ...

7 Panels: Biodiversity and biocomplexity informatics: policy and   80%
implementation science versus citizen science
P. Bryan Heidorn
Proceedings of the second ACM/IEEE-CS joint conference on Digital libraries July 2002
> Biological science is one of the top ten social trends and the twenty-first Century has been defined as "The Age of Biology" [1]. One of the central themes of this age is biodiversity. Biodiversity is the richness of life. Biodiversity includes the variety of genes within one species through the complex interconnection of all life within an environment. One of the grand challenges of the twenty-first century is to document and understand the world's natural heritage. The management of the many k ...

8 Lab report special section: information retrieval research in the   80%
University of Sheffield
Peter Willett
ACM SIGIR F rum December 1997
Volume 31 Issue 2

9 Analogical reasoning for knowledge discovery in a molecular biology   80%
database
Juergen Haas , Jeffrey S. Aaronson , G. Christian Overton
Proceedings of the second international conference on Information and knowledge management December 1993

10 The human genome project and informatics   80%
Karen A. Frenkel
Communications of the ACM November 1991
Volume 34 Issue 11

11 Location-based services and mobile computing: algorithms: A road   77%
network embedding technique for k-nearest neighbor search in moving
object databases
Cyrus Shahabi , Mohammad R. Kolahdouzan , Mehdi Sharifzadeh
**Proceedings of the tenth ACM international symposium on Advances in
geographic information systems** November 2002
  A very important class of queries in GIS applications is the class of K-Nearest Neighbor
  queries. Most of the current studies on the K-Nearest Neighbor queries utilize spatial
  index structures and hence are based on the Euclidean distances between the points.
  In real-world road networks, however, the shortest distance between two points
  depends on the actual path connecting the points and cannot be computed accurately
  using one of the *Minkowski* metrics. Thus, the Euclidean distance may no ...

12 Algorithms on Stings, Trees, and Sequences: Computer Science and   77%
Computational Biology
Dan Gusfield
ACM SIGACT News December 1997
Volume 28 Issue 4

13 Invited papers: Mining the human genome using virtual reality   77%
Bram Stolk , Faizal Abdoelrahman , Anton Koning , Paul Wielinga , Jean-Marc Neefs ,
Andrew Stubbs , An de Bondt , Peter Leemans , Peter van der Spek
**Proceedings of the Fourth Eurographics Workshop on Parallel Graphics and
Visualization** September 2002
  The analysis of genomic data and integration of diverse biological data sources has
  become increasingly difficult for researches in the life sciences. This problem is
  exacerbated by the speed with which new data is gathered through automated
  technology like DNA microarrays. We developed a virtual reality application for
  visualizing hierarchical relationships within a gene family and for visualizing networks
  of gene expression data. Integration of other information from multiple databases with
  th ...

14 Data exploration: HD-Eye: visual clustering of high dimensional data   77%

Alexander Hinneburg , Daniel A. Keim , Markus Wawryniuk
**Proceedings of the 2002 ACM SIGMOD international conference   n Management
f data** June 2002

> Clustering of large data bases is an important research area with a large variety of
> applications in the data base context. Missing in most of the research efforts are
> means for guiding the clustering process and understanding the results, which is
> especially important for high dimensional data. Visualization technology may help to
> solve this problem since it provides effective support of different clustering paradigms
> and allows a visual inspection of the results. The *HD-Eye* (high-dim. e ...

15 Research session: data warehousing and archive: Archiving scientific   77%
data

Peter Buneman , Sanjeev Khanna , Keishi Tajima , Wang-Chiew Tan
**Proceedings of the 2002 ACM SIGMOD international conference on Management
of data** June 2002

> We present an archiving technique for hierarchical data with key structure. Our
> approach is based on the notion of timestamps whereby an element appearing in
> multiple versions of the database is stored only once along with a compact description
> of versions in which it appears. The basic idea of timestamping was discovered by
> Driscoll *et. al.* in the context of persistent data structures where one wishes to track
> the sequences of changes made to a data structure. We extend this idea to deve ...

16 General applications: Complex and interconnected systems: optimistic   77%
parallel simulation of a large-scale view storage system

Garrett Yaun , Christopher D. Carothers , Sibel Adali , David Spooner
Proceedings of the 33nd conference on Winter simulation December 2001

> In this paper we present the design and implementation of a complex view storage
> system model that is suitable for execution on a optimistic parallel simulation engine.
> What is unique over other optimistic systems is that reverse computation as opposed
> to state-saving is used to support the rollback mechanism. In this model, a hierarchy
> of view storage servers are connected to an array of client-side local disks. The term
> *view* refers to the output or result of a query made on the part of ...

17 A proposed undergraduate bioinformatics curriculum for computer   77%
scientists

Travis Doom , Michael Raymer , Dan Krane , Oscar Garcia
**ACM SIGCSE Bulletin , Proceedings of the 33rd SIGCSE technical symposium on
Computer science education** February 2002
Volume 34 Issue 1

> Bioinformatics is a new and rapidly evolving discipline that has emerged from the
> fields of experimental molecular biology and biochemistry, and from the the artificial
> intelligence, database, and algorithms disciplines of computer science. Largely because
> of the inherently interdisciplinary nature of bioinformatics research, academia has
> been slow to respond to strong industry and government demands for trained
> scientists to develop and apply novel bioinformatics techniques to the rapidly-growi ...

18 Efficient algorithms for document retrieval problems   77%
S. Muthukrishnan
**Proceedings of the thirteenth annual ACM-SIAM symposium on Discrete
alg rithms** January 2002

> We are given a collection D of text documents $d1,...,dk$, with $\Sigma i = n$, which may be

preprocessed. In the document listing problem, we are given an online query comprising of a pattern string p of length m and our goal is to return the set of all documents that contain one or more copies of p. In the closely related *occurrence listing* problem, we output the set of all *positions* wi ...

19 Distributed query evaluation on semistructured data   77%

Dan Suciu
ACM Transactions on Database Systems (TODS) March 2002
Volume 27 Issue 1

Semistructured data is modeled as a rooted, labeled graph. The simplest kinds of queries on such data are those which traverse paths described by regular path expressions. More complex queries combine several regular path expressions, with complex data restructuring, and with sub-queries. This article addresses the problem of efficient query evaluation on distributed, semistructured databases. In our setting, the nodes of the database are distributed over a fixed number of sites, and the ...

20 NBDL: a CIS framework for NSDL   77%

Joe Futrelle , Su-Shing Chen , Kevin C. Chang
Proceedings of the first ACM/IEEE-CS joint conference on Digital libraries January 2001

In this paper, we describe the NBDL (National Biology Digital Library) project, one of the six CIS (Core Integration System) projects of the NSF NSDL (National SMETE Digital Library) Program.

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1 Book reviews: Introduction to constraint databases   77%
Bart Kuijpers
ACM SIGMOD Record September 2002
Volume 31 Issue 3

2 Pattern discovery and forecasting: An iterative strategy for pattern   77%
discovery in high-dimensional data sets
Chun Tang , Aidong Zhang
Proceedings of the eleventh international conference on Information and
knowledge management November 2002
   High-dimensional data representation in which each data item (termed target object) is
   described by many features, is a necessary component of many applications. For
   example, in DNA microarrays, each sample (target object) is represented by thousands
   of genes as features. Pattern discovery of target objects presents interesting but also
   very challenging problems. The data sets are typically not task-specific, many features
   are irrelevant or redundant and should be pruned out or filtered for the ...

3 A cost model for query processing in high dimensional data spaces   77%
Christian Böhm
ACM Transactions on Database Systems (TODS) June 2000
Volume 25 Issue 2
   During the last decade, multimedia databases have become increasingly important in
   many application areas such as medicine, CAD, geography, and molecular biology. An
   important research topic in multimedia databases is similarity search in large data sets.
   Most current approaches that address similarity search use the feature approach,
   which transforms important properties of the stored objects into points of a high-
   dimensional space (feature vectors). Thus, similarity search is transformed ...